In the Claims:

Cancel claims 1-80 and replace them with the following claims.

81. (New) A method of screening compositions for opioid activity comprising the steps of a) contacting a test cell that expresses a human KOR-3 splice variant polypeptide comprising at least five consecutive amino acid residues encoded by nucleotides located between exon 1 and exon 2 of the human KOR-3 gene with the composition in an amount sufficient to exert a physiologic effect when an opioid agonist or antagonist of said splice variant polypeptide is present in the composition; b) measuring the physiologic effect of the composition on the test cell.

82. (New) The method according to claim 81, where the composition is selected from the group consisting of synthetic combinatorial libraries of small molecule ligands, eukaryotic whole cell lysates or extracts, or media conditioned by cultured eukaryotic cells.

83. (New) The method according to claim 81, where the physiological effect is measured by changes in the levels of neuroendocrine hormones.

84. (New) The method according to claim 83, where the hormone is selected from the group consisting of prolactin, growth hormone, gonadotropin-releasing hormone, adrenocorticotropin, corticotropin-releasing factor, luteinizing hormone, follicle stimulating hormone, testosterone or cortisol.

85. (New) The method according to claim 81, where the physiological effect is measured by determining the binding affinity of the opioid agonist or antagonist for the splice variant polypeptide.

86. (New) A method of screening compositions for opioid binding activity comprising the steps of a) contacting a composition with a test polypeptide comprising a human KOR-3 splice variant polypeptide, wherein the KOR-3 splice variant polypeptide comprises at least five consecutive amino acid residues encoded by nucleotides located between exon 1 and exon 2 of the human KOR-3 gene; b) contacting the test polypeptide with an amount of an opioid sufficient to measurably bind the test polypeptide; e) measuring the binding of the composition and the opioid; and f) comparing test polypeptide binding of the composition to that of the opioid, where determination of binding of the composition is expressed relative to that of the opioid.

87. (New) The method according to claim 86, where the composition is selected from the group consisting of synthetic combinatorial libraries of small molecule ligands, eukaryotic whole cell lysates or extracts, or media conditioned by cultured eukaryotic cells.

88. (New) A method of screening compositions for opioid activity comprising the steps of a) contacting a test cell that expresses a human KOR-3 splice variant polypeptide comprising at least five consecutive amino acid residues encoded by nucleotides located between exon 1 and exon 2 of the human KOR-3 gene with the composition in an amount sufficient to exert a physiologic effect when a KOR-3 opioid agonist or antagonist is contained in said composition; b) contacting a control cell that expresses said KOR splice variant polypeptide with a KOR-3 opioid agonist or antagonist; c) separately measuring the physiologic effect of the control cell and test cell; and d) comparing the physiologic effect of the composition to the physiologic effect of the opioid, where determination of a physiologic effect of the composition is expressed relative to that of the opioid.

89. The method according to claim 81, wherein the splice variant polypeptide is human KOR-3A, consisting essentially of the amino acid residues depicted in SEQ ID NO: 6.

90. The method according to claim 81, wherein the splice variant polypeptide is human KOR-3D, consisting essentially of the amino acid residues depicted in SEQ ID NO: 7.

91. The method according to claim 86, wherein the splice variant polypeptide is human KOR-3A, consisting essentially of the amino acid residues depicted in SEQ ID NO: 6.

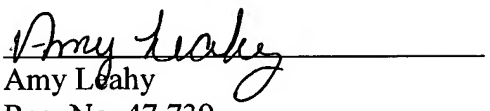
92. The method according to claim 86, wherein the splice variant polypeptide is human KOR-3D, consisting essentially of the amino acid residues depicted in SEQ ID NO: 7.

93. The method according to claim 88, wherein the splice variant polypeptide is human KOR-3A, consisting essentially of the amino acid residues depicted in SEQ ID NO: 6.

94. The method according to claim 88, wherein the splice variant polypeptide is human KOR-3D, consisting essentially of the amino acid residues depicted in SEQ ID NO: 7.

The Assistant Commissioner is hereby authorized to charge any additional fees that may be required by this transmittal, or to credit any overpayment, to **Deposit Account No.:50-0320**.

Respectfully submitted,
FROMMER LAWRENCE & HAUG LLP
Attorneys for Applicant



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